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General Physiology is the study of biological mechanisms through analytical investigations, which decipher the molecular and cellular mechanisms underlying biological function at all levels of organization.

The mission of the *Journal of General Physiology* is to publish articles that elucidate important biological, chemical, or physical mechanisms of broad physiological significance.

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Cover picture: (Top) Schematic representation of classical signaling by M_1 muscarinic receptors (M_1R). (Bottom) FRET measurements of individual signaling steps (dots) compared to predictions of a kinetic model of the M_1R signaling cascade (numbered curves). (1) Agonist binding reported by intramolecular FRET. (2) G protein binding to the receptor, FRET from M1R-CFP/ Gβ-YFP. (3) Nucleotide exchange, FRET from $G\alpha_q$-CFP/ Gβ-YFP. (4) $G\alpha_q$ binding to PLC, FRET from $G\alpha_q$-CFP/ PLC-YFP (see article by Falkenburger et al., 81–97).

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Cover picture: Gating energy changes at the acetylcholine receptor transmitter binding site were estimated from the kinetics of spontaneous currents. (Top) Left, unliganded *Torpedo* receptor; right, the α_ε binding site (right: yellow, loop A; green, loop B; purple, loop C; white, complementary subunit). (Bottom) Single-channel currents from unliganded receptors with the mutation αY190R. Each cluster of openings (down) is from one receptor (see article by Purohit and Auerbach, 321–331).

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Cover picture: Composite of figures from *Perspectives on molecular dynamics and computational methods.* (Top) All-atom simulation of single-channel currents through Kv1.2 (see Perspective by Dror et al., 555–562). (Bottom left) Two symmetric modes of the prokaryotic potassium channel KcsA (see Perspective by Bahar, 563–573). (Bottom right) Energy landscape calculated in simulation of state transitions of KCNQ1 (see Perspective by Silva and Rudy, 575–581).